NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CAR §1.821 - §1.825 for the following reasons(s):

1. This application clearly fails to comply with the requirements of 37 CAR §1.821 - §1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990, and at 55 FR 18230, May 1, 1990. 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" [] as required by 37 CAR §1.821(c). 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CAR §1.821(e). 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of X the computer readable form does not comply with the requirements of 37 CAR §1.822 and/or §1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing". 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CAR §1.825(d). 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CAR §1.821(e).

APPLICANT MUST PROVIDE:

[]

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as were as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CAR §1.821(e) or §1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT:

For Rules Interpretation, call (703) 308-1123 For CRF Submission help, call (703)308-4212 For Patentin Software help, call (703) 557-0400

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE.

1645

RAW SEQUENCE LISTING

DATE: 09/06/2000

PATENT APPLICATION: US/09/446,677

TIME: 11:01:37 .

Input Set : A:\Birkell.txt

Output Set: N:\CRF3\09062000\I446677.raw

SEQUENCE LISTING

```
(1) GENERAL INFORMATION:
            (i) APPLICANT: BIRKELUND, Svend
                            CHRISTIANSEN, Gunna
     6
                            HEBSGAARD PEDERSEN, Anna-Sofie
                            MYGIND, Per
     8
                            KNUDSEN, Katrine
           (ii) TITLE OF INVENTION: SURFACE EXPOSED PROTEINS FROM CHLAMYDIA
     9
    11
                                     PNEUMONIAE
    12
          (iii) NUMBER OF SEQUENCES: 30
    14
           (iv) CORRESPONDENCE ADDRESS:
                  (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
    17
                  (B) STREET: 624 Ninth Street, N.W., Suite 300
    18
                  (C) CITY: Washington
    19
                  (D) STATE: D.C.
    20
                  (E) COUNTRY: USA
     21
                  (F) ZIP: 20001
     22
             (V) COMPUTER READABLE FORM:
     24
                  (A) MEDIUM TYPE: Floppy disk
     25
                  (B) COMPUTER: IBM PC compatible
     26
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     27
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     28
            (vi) CURRENT APPLICATION DATA:
     30
                  (A) APPLICATION NUMBER: US/09/446,677
C--> 31
                  (B) FILING DATE: 24-Mar-2000
C--> 32
           (vii) PRIOR APPLICATION DATA:
C--> 38
                  (A) APPLICATION NUMBER: PCT/DK98/00266
     35
                   (B) FILING DATE: 19-JUN-1998
     36
                   (A) APPLICATION NUMBER: DK 0744/97
(B) FILING DATE: 23-JUN-1997
     40
          (viii) ATTORNEY/AGENT INFORMATION:
     42
                   (A) NAME: COOPER, Iver P.
     43
                   (B) REGISTRATION NUMBER: 28,005
     44
                   (C) REFERENCE/DOCKET NUMBER: BIRKELUND=1
     45
             (ix) TELECOMMUNICATION INFORMATION:
     47
                   (A) TELEPHONE: 202-628-5197
      48
                   (B) TELEFAX: 202-737-3528
      49
```

Does Not Comply Corrected Diskette Needed

see pp. 2,4,6

ERRORED SEQUENCES

```
498 (2) INFORMATION FOR SEQ ID NO: 3:
         (i) SEQUENCE CHARACTERISTICS:
500
              (A) LENGTH: 2815 base pairs
501
              (B) TYPE: nucleic acid
502
              (C) STRANDEDNESS: single
503
              (D) TOPOLOGY: linear
504
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DATE: 09/06/2000 TIME: 11:01:37

Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I446677.raw

Enter hord return here to correct.

	1	to correct
506 (ii) MOLECULE TYPE: Genomic DNA	here	70 (
506 (ii) MOLECULE TYPE: GENOMIC SEQ ID NO: 3: 508 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	mmccmc	CAAC TGCTGAAAAT ATA(
TO TOCAL TOTAL TOT	CTGTTT TIGCIG	CARC 1001
E> 510 ATGAARTCGC AATTTTCCTG GTTAGTGCTC TCTTCGACAT TGGCATGTTT TACTAGTTGT 60 TCCA ATGAARTCGC AATTTTCCTG GTTAGTGCTC TCCTAAAAAT ACGACTACTG GAATAGACTA TACTCTGACA	180	
	240	
	300	
	360	••
	420	
	480	
	540	
	600	
	660	
	720	
	780	
	840	
	900	
	960	•
	1020	
523 GGAAACCAAG CITTTCTAAC AATATAGTCC AAGGTACCAC 524 GGGGGGGGG GGGTATCTC CTTTTCTAAC AATATAGTCC TTTCAGCAGA AGCAGGGGAC 525 GGTGGAGCCA TTTCTATACT GGCAGCTGGA GAGTGTAGTC TTTCAGCAAA AAGAAATTCT 526 GGTGGAGCCA TTTCTATACT GCAGTGGA ACTACACCA AAACTACAAA AAGAAATTCT	1080	
524 GGGGGGGGGG GGGATTTTCTATACT GGCAGCTGGA GAGTGTAGTC TTTCAGCAGA AAGAAATTCT 525 GGTGGAGCCA ATTCTATACT GGCAGCTGGA ACTACACA AACTACAAA AAGAAATTCT 526 ATTACCTTCA ATGGGAATGC CATTGTTGCA ACTACACCA CAACTACCACA CAACTACCACC GAAAATTCTG	1140	
526 ATTACCTTCA AIGGARCTGC AAAGATCACG AATTTACGTG CAATATCTGG CAATATCTGG	1200	
	1260	
	1320	
	1380	
	1440	
	1500	
531 GTAACTCTAA CIGCAGGTTC CTCTGTTATT ATGGATGCGG GCACAAGGT 532 TTTACTCAGA CCGCGGGTTC CTCTGTTACT ATTCCTGTAG ACTCTTTAGG CGAGGGTAAG 533 ACAGAGGAGG TCACTTTAAC AGGTCTTTC ATTCCTGTAG ACTCTTAGTGG TCCGATTCTT	1560	
	1620	
	1680	
	1740	
	1800	
	1860	
	1920	
	1980	
	2040	·
541 GGCTTCTGGG CTGCGGGGGT TCGCTTTGCT ATCGGAGGTG CAGCGCAAAC TTGTTCTGGGT		
	2160	
	2220	
		•
545 GGGTTCATAG GTTGTCTCTT MACCCACGTC AGTAATGATC TGAAGACAAA GTATACCGTCCTC	2340	
		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
		•
	2815	
552 GATCCCAAAT GCACAGGCCTT GCAAGTGCGT GCAGGCAGTC ACTACGCCTT CTATAATGTZ 553 AACTTAGCAC GACAGGCCTT TGTCTTTGAA GTTCGTGGAT CCTCACGGAT TTATAATGTZ 554 TTTGAAGTGC TCGGCCAGTT TGTCTTTGAA GTTCTCAT GTCTCAGAAA TTCTG	2013	
553 AACTTAGGGC TCGGCCAGTT TGTCTTTGAA GTTCGTGGAT CCTCAGGAA TTCTG 554 TTTGAAGTGC TCGGCCAGTT TGTCTTTGAA GTTCGTGGAT CCTCAGAAA TTCTG 555 GATCTTGGGG GTAAGTTCCA ATTCTAGGAG CGTCTCTCAT GTCTCAGAAA TTCTG 555 GATCTTGGGG GTAAGTTCCA ATTCTAGGAG CGTCTCTCAT GTCTCAGAAA TTCTG		
555 GATCTTGGGG GTARGITECT NO: 5: 743 (2) INFORMATION FOR SEQ ID NO: 5:		

DATE: .09/06/2000 TIME: 11:01:37

Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I446677.raw

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 3052 base pairs (B) TYPE: nucleic actu (B) Type: nucleic actu (C) STRANDEDNESS: single (D) Topology: linear (D) Topology: linear (E) (I) MOLECULE TYPE: Genomic DNA (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 5: ATGGGATTTT CGCTCTCGGG ATTTCCTCTA GTTTTTCTT TARCATTGCT CTCAGTCTC (G) CACACTTCTT TGAGTCCTAC TARCAGTTTCT TTARCACCGG AAGATAGTTT TCATGGGGT (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 5: ATGGGATTT CGCTCTCGGG ATTTCCTCTA GTTTTTTCTT TARCATTGCT CTCAGTCTC (G) GACACTTCTT TGAGTCCTAC TARCAGTTTCT TARCACCGG AAGATAGTTT TCATGGGGT (T) AGGGAATG TGACACTTCC AGGGATCT CAAGGATCT CAATGGATC (S) TCAGGAATG TGACCATTGCA AGGAATCAT CAAGGATCT CAATGAATAC CCTTACTGGT (S) TCAGGAATG TGACCACTCTC TATTATATCT CAAGGATAT ATTTTATATA TATTTCCTCA (S) TCAGGAATG TGACCACTCTC TATTATATCT CACCAGATC CCCAAGATC (C) CTCTATTCAA AGAAGGGGC TATACTTTGT TGCCAAGATC CCCAAGATC TATGCCTTTA AACAATTAT TAGGGCATG GGCACGATTT (S) CAAAGTAAGA CTAAAGGCGA GGCACTTTTTA AACAATTATG TAGGGGAACAC (S) CACACTACAGA TACCAGTAAA TCAGGCGAGA ATAAGATTAT CACAAAATAC TCCCAAGAAT (G) CATTTCCAGA AAAATCAGCGA GAATCACTTTGCACAAATACAC (G) CTTATTCCAG AAAATCAGCGA ATAAGATTTA TCACACAAATAC TCCCAAGAAT (G) CTATTTCCAG AAAATCAGGCA ATCCCAATTATGAT TCACACAAATAC (G) CTATTTCCAGA AAAATCAGGCA TACCCATTTGTAT CACAAAATAC TCCCCAAGAT (G) CTATTTCCAGA AAAATCAGGCA TACCCATTGA AGGGAGGGC TCTCTTGTT (G) GATCCCCTT CAGGAGATG TACCTCCATT CCTATTGTA CACAAAATAC (G) CTATTTCCAGA AAAATCAGGCA CATTTATGATA TTACACAGAAA TCCCCAACTATGAT (G) CTATTTCCAGG AAAATCAGGC ATTCCAATAATA TACCATAATA TACCATAGAA (G) CTATTTCCAGG AAAATCAGGC ATTCCAATAATA TACCATAATAC CACCAACATAC (G) CTATTTCAAGAAT CATTCCAAGAA TACCACAGA AGGGGAAAT CACCAACTAC (T) AGCACACTCT CAGAGAGTG TACCCCAATTGATA TACCATAACC (T) AGCACAATTA CATTCCAAGA AACCGGCA CACTTTATACC AAAATCACGAA (T) AATTCAGAAGA CACTAAATCC CATTCCAATAA TACCACAGAA AAACTCACAA (T) AAACACAGGAAC CATTACCAATAA TACCACAGAA AAACTCACAA (T) AAACACAGGAAC CAAACACTAC CAACACTCCC TACCAACTACC CAATTAACAC (T) AAAAAACAAA TACCAGGAAC CAACACTACCAA CAACACCACCAACAACACCACAACAACACCACAACA	Output See.	
(C) STRANDEDNESS: SINGLE (D) TOPOLOGY: linear (A) SQUENCE DESCRIPTION: SEQ ID NO: 5: (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X2) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X3) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X4) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X5) AGROCATTIT CGCTCTGGGG ATTTCCTCTA GTTTTTCTT TAACATTGCT CTCAGTCTTC (X5) AGROCATTT TGAGTGCTAC TAGGAGTTCT TTAACACCCAGA AAGATACTTT TCATGGAGAT (X5) GACACTTCTT TGAGTGCTAC TAGGAGTTCT TTAACACCCAGA AAGATACTTT TCATACTGACC (X6) AGROCATACAA AGGAAGGGC CTATAAAATA AAGCCTGCTT CAAATGGACC (X6) GACACTACAA AGGAAGGGC CTATAAATACT CAAGCCTGGGG ATTTTAAAGA ACAGGAGTC (X6) GAGACTACAA AGGAAGGGC CTATATTCTTC AGGACACAC GGCAGGTTT (X6) GGAACTACAA AGGAAGGGC CTATACTTGT TGCCAGAGAT CTATAAGAA ACAGCACAC (X6) CAAAGTACAA AGGAAGGGC TTATTTCTCAGAGACCCC ACTTTTGGAG GTCCTATCAGA TGCAACACAC (X6) CAAAGTACAA CTAAAGCCCC ACTTTTGGAG GTCCTATCCAA TTCCTCAGGT (X6) CAAAGTACAA AAAATGCACCT ATTGCTCCTTA AACAATTACT TACATACAA ATCCCCAAACACCACACCT CTTCTATACAA AAAATGACACT TACCAACACACACACACACACACACACACACACA	CROWENCE CHARACTERISTICS:	
(C) STRANDEDNESS: SINGLE (D) TOPOLOGY: linear (A) SQUENCE DESCRIPTION: SEQ ID NO: 5: (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X2) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X3) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X4) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X5) AGROCATTIT CGCTCTGGGG ATTTCCTCTA GTTTTTCTT TAACATTGCT CTCAGTCTTC (X5) AGROCATTT TGAGTGCTAC TAGGAGTTCT TTAACACCCAGA AAGATAGTTT TCATGGAGAT (X5) GACACTTCTT TGAGTGCTAC TAGGAGTTCT TTAACACCCAGA AAGATAGTTT TCATGGAGAT (X6) GACACTACAA AGGAAGGGC CTATAAAATA AAGCCTGCTT CAAATGGACC (X6) GAGACTACAA AGGAAGGGC CATATAAATA AAGCCTGCTT TAATATGACCAAACACACACACACACACACACACACACAC	745 (1) SEVOLUTE 3052 base pairs SEC P. 7	
(C) STRANDEDNESS: SINGLE (D) TOPOLOGY: linear (A) SQUENCE DESCRIPTION: SEQ ID NO: 5: (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X2) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X3) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X4) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (X5) AGROCATTIT CGCTCTGGGG ATTTCCTCTA GTTTTTCTT TAACATTGCT CTCAGTCTTC (X5) AGROCATTT TGAGTGCTAC TAGGAGTTCT TTAACACCCAGA AAGATAGTTT TCATGGAGAT (X5) GACACTTCTT TGAGTGCTAC TAGGAGTTCT TTAACACCCAGA AAGATAGTTT TCATGGAGAT (X6) GACACTACAA AGGAAGGGC CTATAAAATA AAGCCTGCTT CAAATGGACC (X6) GAGACTACAA AGGAAGGGC CATATAAATA AAGCCTGCTT TAATATGACCAAACACACACACACACACACACACACACAC	746 (R) TYPE: nucleic acid	
(i) MOLECULE TYPE: Genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (xi) SEQUENCE DESCRIPTION: AAGGATGTT COLORS AFTER TOTAL AAGCATGTT TOTAL AAGCATGTT TOTAL AAGCATGTT TOTAL AAGCATGTT TOTAL ATTICATED AAGCATGTT TOTAL AAGCATGTT TOTAL AAGCATGTT TOTAL AAGCATGTT TOTAL AAGCATGTT TOTAL AAGCATGT TOTAL AAGCATGTT TOTAL AAGCATGT TOTA	C CODYNDEDNESS: SIDGIE	
(ii) MOLECULE TYPE: Genomic DNA: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: ATCAGATTT GCCTCTGCGG ATTTCCTCTA GTTTTTCTT TAACATTGCT CTCAGTCTTC AGCAGATTT GCCTCTGCGG ATTTCCTCTA GTTTTTCTT TAACATTGCT CTCAGGAGT T55 ATCAGAAGTC TAGCAGCTTC TATAAATGTT CAAGCTGGGG ATGTCTATAAG CCTTACTGGT T75 AGTCAGAAGTC TAGCAACGTTC TATAAATGTT CAAGCTGGGG ATGTCTATAAA CCCAGAACTTC CAAGAACGTC CAAGAACGTC CAAGAACTTC CAAGAACTTC CAAGAACTTC CAAGAACTACA AGGAAAGTC TAGCAGTAAATA AGCACTGCTA TATTTAATAA TATTTCCTCA 300 TCAGGAAGTC TAAGAAGGGC TGTACTTTGT TGCCAAGAAC GCCACGTTTT TGAGCAAGAC GCCCCGGA ATATTAAAGA ACAGAGGATT TAGCCTCTTA AACAATAAC CTCAAGCAAC GCCACGTTTT TGAGCAAGAAC CTCATATTCAA AAAATCACAC TATTCTTCTCA AACAATAAC ATTTCAATACA ACAGAGAACTAC ACAAGAACTAC ACAAGAACAC ACTTTTTGGAG GTGCTACCAC TTCTTCAGGT AGCAACTAC ACAAGAACAC ACTTTTGGAG GTGCTACCAC TTCTTCAGGT ACCAAAATAC TCCCACACACAC ACTTTTGGAG GTGCTACCAC TTCTTCAGGT ACCAAAATAC TCCCAACACAC ACTTTTGGAG GTGCTACCAC TCTTCTCAGGA AAAATCAGCA ATTCACACACA ATTCACACAAA TCCCCACACAC ACTTTTCTCAGA CACAAAATAC TCCCAACACAC ACTTTTTGGAG GTGCTACCAC TCTTTCTCAGG AAAATCAGC ACTTCACTCT CAGGAGACTA CACCAACACAC TCCCAACACAC TCCCAACACAC TCCCACACAC TCCCACACACA	(D) TOPOLOGY: linear	
755 ATGGARTTE GESCRIFTION: STATEMENT TAACATTCCT CTCAGTCTTC 755 ATGCGATTTE GECTCTEGG ATTTCCTCTA GTTTTTCTT TAACATAGTT CATCAGAGAT 756 GACACTTCTT TAGGTGCTAC TACGATTCT TTAACCCAA AAGATAGTT CATGAGAGAT 757 AGTCAGAATG CAGAACGTC TATAAATGT CAAGGAGGA ATGCTATAGA 758 GATGTCAGAATG CAGAACGTC TATAAATGT CAAGGAGGA AAGATCAT 759 TCAGGAAGGTC TACGATTCG AGGAAATCAT CATGGGTATA ATTTTAATAA ATTTTCCTCA 750 GGAACCATCA AAGAAGGGC GTACTTTGT TGCCAAGAAC GCACGATTT 760 GGAACCATCA CAGAAGGGC TGTACTTTGT TGCCAAGAAC GCACGATTT 761 CTTGGGTTC CCACGCTCC TTTTATTCAG AGCCCCGGAG ATATTAAAAA ACGCACACA 762 CTCTATTCAA AAAATACACT TATGCTCTTA AACAATAAT TATGCGCTTT TCAACAAAAC 763 CAAAGATAAA ACAACACAC ACTTTTGGA GATTCAATATA TAGCACAAAAC 764 GATTCCGCT CTTTCTATCA GAATCCACCA ACTTTTGGA GTGCTATCA TCTCTCAGGT 765 GATTCTGGAG GGCTTTGTA 766 GGTTCTGGA GGCCCTCTC ATTAAAATC CCCCAAGAAT 767 TATGTCTGGA GAAATCAGC ATTGCACTAAA TCAGCACACA 768 CTTCCCATTG AAAAAACCA TCCCAAGTAT GCTCATATGT AGCAAAATAC 769 TTAGTCTTTG AAAAAACCA TCCCAAGTT GCTCAATAAATA TATGATCAGAA TCCTTATGTT 760 ACCATCTCTT CAGGAAGAAC TCCCAATTA TACAATAATA TATCAATAGC AAATACCAG 767 TATTTTGGAG GACCAAACT TCCCAATAT GCTCATAATA TATCAATAGC AAATACCAG 768 CTTCCCACTT CAGGAAGAACCA TCCCAATTA TACAATAATA TATCAATAGC AAAATTCGCAA 769 TTAGTCTTTG AAAGAAACCA TCCCAATTA TACAATAATA TATCAATAGC AAAATTCGCAA 770 ACCATCTCTT CAGGAAGAACCA TACCCAATTA TACAATAATA TATCAATAGC AAAATTCGCAA 771 AATTTAGGTG GAGCTATTCC CATTGATACT GCAAGAAATA 772 TATCAAAATA CATTCCAAGA AACCGAACA GCCAAATAAATA 773 TTACAAAATA CATTCCAAGA AACCGAACA GCCAAATAAATA 774 GAGCAATTAA CACCAAGGAC CATACCTTTT TACAGAAAAA AACCGAACAA 775 ATAAAAATAA ATTACAACA CCCTCAAAAA TTCCCCAATTAATA AACCGAACAA 776 AGGAATTTAA CACCAAGGAA TACCAGACA CATTCCTTAT TACAACAACAAAAAAAAAA	The second of th	
755 ATGCGATTTT CGCTCTGCGG ATTICCTCT TRACCCCAG ANGARACTT TCATGAGGAT 120 756 GACACTTCTT TGAGTGCTAC TACGATTCT TTAACCCCAG ANGARACTT CCATACTGGT 180 757 AGTCAGAATG CAGAACGTC TATATATGT CAAGCTGGGG ATGTCTATAG CCTTAACTGACT 758 GATCACAA AGCAAGGGC CGATAACTCT CGATTAAATA AAGCCTCCTT CAATGTGACC 759 TCAGGAATG GACGTTCC AGGAAATCAT CATGCTATAATA AAGCCTCCTT CAATGTGACC 760 GGAACTACAA AGGAAGGGC TGTACTTGT TGCCAAGGATC CTCAAGCAAC GGCACCGTTT 760 GGAACTACAA AGGAAGGGC TGTACTTGT TGCCAAGGAT CTCAAGCAAC GGCACCGTTT 761 TCTGGGTTCT CCACCGCTCT TTTTATTCAG AGCCCCGGAG ATATTAAAGA ACAGGGATGT 762 CTCTATTCAA AAAATGCACT TATGCTCTTA AACAATTATT TAGTCCGAAC GGCACCTAC 763 CAAAGTAAGA CTAAAGGCGG AGCTATTAGT GGGGCGAATT TATGATACAGA TAGCCAAGAAAC 764 GATCCGTCT CTTTCTATACG GAGCCACCAC ACTTTTGGAG GTGCTATCCA TTCTCAGGT 765 CCCCTACAGA TTGCAGTAAA TCACGAGGAG ATAAGAATTC CACAAAAAAC TCCCATAATG GTGCGGGAAC TATGACTACAA TCCCAAGTA CCCAATGAAATAC TCCCAATGAA TCCCAAGTA ACAATAACAG ACAATAAACAG ATTACACAACT TCCATAATG GTGCGCGAG CCATTTATCC TAGGAAAACA TTCCAATATG GTGCGCGAG CAATTAACACAG ACACCAATAACACAG AACACAATAAC CAACACACTAC CAAGGAACAAC TTCCATAATA GGGCGGGGAC CATTTATCC AAAATAACAG AACCACGAACAAC TTCCATAATA GGGCGGGAG CAATTAACACAG AACCAGGAAAAC AACCACCACTAC TACCACTATT ATCAATAATA TATCATATAC AAAATACAG AACCACGGAC AACTTCAATAC CAATGAAACA TTCCAATAATACAG GACCAATACACAG AACCAGGGAAA ACACCACCACTACACACTACAAAACCA CAATCACAAAC CAATCACAAT CCTCTAATAC GAGCAGAAAA GACCACTCTAA AACACACCAC AACTTCAAAAC CCCCAATGAA AACACCACCAATGAAACAC AACACCACACAC AACACTCAAAACAC CAAACCACCACACC AACTTCCAAAACAC AACACCACACAC AACACCACACAC AACACCAC	751 (II) MODES DESCRIPTION: SEQ ID NO: 5:	60
756 GACACTTCTT TRAGACTACT CAAGACGTTC TATATAGTT CAAGCTGGG ATGCTATAG CCTTACTGGT 150 758 GATGTCTCAA TATCTAACGT CGATAACTT GCATTAAATA AAGCCTGCTT CAATGTACC 240 759 TCAGGAAGTG TGACGTTCGC AGGAAATCAT CATGGGTTAT ATTTTAATAA TATTTCCTCA 360 759 TCAGGAAGTG TGACGTTCGC AGGAAATCAT TGCCAAGGAT CTCAAGGAAG GGCACCTTT 760 760 GGAACTACAA AGGAAGGGGC TGTACTTTGT TGCCAAGGAT CTCAAGGAAG ACAGGGATGT 420 761 TCTGGGTTCT CCACGCTCT TTTTATCAG AGCCCCGGAG ATATTAAAGA ACAGGGAACT 480 762 CTCTATTCAA AAAATGCACT TATGCCTTAA AACAATTAT TAGTGCGTTT TGAACAAAAC 480 763 CAAAGTAAGA CTAAAGGCGG AGCTATTAGT GGGGCGATT TTATTATAGT AGGCACCAC ACTTTTGGAG GGCTATCCA TTCCTCAAGGT 660 764 GATCCGTCT CTTTCTATCA GAATGCAGC ACTTTTGGAG GGCTATCCA TTCCTCAGGT 660 765 CCCCCACAGA TTCCCGATAAA TCAGGCAGGA ATAAGATTTG CACAAAATAC TGCCCACAGAT 720 766 GGTCTTCGAG GGGCTTTGTA CTCCGATGCT GATATTGATA TTGATCAGAA TGCTTATGTT 720 767 CTATTTCGAG AAAATGAGGC ATTGACTACT GCTATAGGTA AGGGAGGGGC TGTCTGTTG 780 768 CTTCCCACTT CAGGAAGTGA TACCCACTACT CCTATATGT ACAGGAAGACA 760 769 TTAGTCTTTC AAAGAAACCA TTCCCATATG GTTATGGAA ACCAGGAAC 771 AATTTAGGTG GAGCTATTCC CACTCAATT GGTGGGGAG CCATTTATC CAAGCAAAACCA 772 AAATTAAGGTG GAGCTATTCC CACTCAATT GGTGGGGAG CCATTTATC AAAATCCAA 773 AATTAGGTG GAGCTATTCC CATTCAATCT GGAGGGGAG CATTCACTAT AACAATATA TACCATACAG GAACCCTACT AACCCACTCT TACCAGGAAA AACCGGACA ACCCAACCTAT CATCCAATCA AACCCGAAA 774 AGACCCAATTA CATTCCAAGC AAATCCAC GAATTACAG GAGGAGAAA AACCGGACA ACCCAACCTAT AACACACCAC CAACCCTAC CATCCAACCTAT AACACAGGAAA AACCGGACA AACACAGGACA AACCAGACAAC CAACCCACCTAT TACCAACCTAC CATCCAACCTAC CATCCAACCTAC CAACCCACCTAC CAACCCACC CAACCCACC CAACCCACCACCACCAC	753 (XI) SECURITY CONTINUES ATTICCTOR GITTITTOTT TRACKITGOT CICAGOTT	
757 AGTCAGAATG CAGACGTC COATAACTCT GCATTAATA AGCCTGCT CAATGTACC 240 758 GATGCTCAA TATCTAACGT COATAACTCT GCATTAATA AGCCTGCT CAATGTACC 300 759 TCAGGAAGTG TGACGTTCGC AGGAARTCAT CATGGGTTAT ATTTTAATAA TATTTCCTCA 300 760 GGAACTACAA AGGAAGGGC TGTACTTTGT TGCCAAGGAC CTCAAAGCAAC GGCACGTTT 360 761 CTGGGTCT CCACGCTCT TTTATTCAG AGCCCCGGGA TATTAAAGA ACAGCAACTAC 480 762 CTCTATTCAA AAAATGCACT TATGCTCTTA ACAATTATG TAGCCGCTT TGAACAAAAC 480 763 CAAAGTAAGA CTAAAGGCGG AGCTATTTGGT GGGGCGAATT TTGCACGAAT 760 764 GATTCCGTCT CTTTCTATCA GAATGCAGC ACTTTTGGAG GTGCTATCA TGCCCAAGAAT 760 765 CCCCTACAGA TTGCAGTAAA CACGCAAGA ATAAGATTTG CACAAAATAC TGCCAAGAAT 760 766 GGTCTTGGAG GGCTTTTAT CTCCGATGGT GATATGATA TTGATCAGAA TGCCTAAGAT 760 767 CTTTTCTGAG AAAATGAGGC ATTGCACTATA TCCCCAAGAAT TCCCCAAGAT 760 768 CTTCCCACCT CAGGAAGTAG TACCCAATTATG GCTTATTGTA TTGTTCTGTGT 780 769 TTAGTCTTTC AAAGAAACCA TTCCATAATG GGTGCGGAG CCATTTATCC TAGGAAACT 780 769 TTAGTCTTTC CAGGAGGTC TACCCATAATG GGTGCGGAG CCATTTATCC TAGGAAACT 770 769 TTAGTCTTTC CAGGAGGTC TACCCATAATG GGTGCGGAG CCATTTATCC TAGGAAACT 771 769 TTAGTCTTTC CAGGAGGTC TACCCATAATG GGTGCGGAG CCATTTATCC TAGGAAACT 772 760 AGCACCTCT CAGGAGGTC TACCCATAATG GGTGGGGAGA TCAGTTATC AGCAGAAAT	755 ATGCGATTT TCAGTGCTAC TACGATTTCT TTAACCCCAG AAGATAGTTT TCAGGGAT	
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765 CCCCTACAGA TICCAGTAGA CACCGATGAT ACCCCAGATGAT ATTGATCAGAA TGCTTATGATT 766 GGTTCTGGAG GGGCTTTGTA CTCCGATGGT GATATTGATA AGGGAGGGG TGTCTGTTGT 780 767 CTATTTCGAG AAAATGAGGC ATTGACTACT GCTATTGTGA CTTTCTCTGA CAATAAACAG 768 CTTCCCACTT CAGGAAGTAG TACTCCAGATT CCTATATGT AGGGAGGGG CAATTATGC TAGGAAACCA TTCCATAATG GGTGGCGGAG CCATTTATGC AAATTCCGAA 770 AGCATCTCTT CAGGAGGTCC TACTCTATTT ATCAATATA TATCATATGC AAATTCGCAA 771 AATTTAGGTG GAGCTATTCC TACTCTATTT ATCAATATA TATCATATGC AAATTCGCAA 772 GGAACAATTA CATTCCAGAG AAACCGGACG AGCTTACCGT TTTTGAATG CACCCACTT 1080 772 GGAACAATTA CATTCCTAGAGC AGATGGGTCT TCTGGAGAAA AGAGTCCTATA AGAATTTAT 1140 773 TTACAAAATG CTAAATTCCT GAAATTACAG GCGAGAAAAT GATCCTATA ACCCAATTGA ATATCAACGA AGATCCTATA ACCCAATTGA ATATCAACGA AAACCAGCACT 1200 775 AATAAAAGAGT ACACAGGGAC CAAACTCTT TCTGGAGAAA AGAGTCTAGA AAACCACCGAA 777 AAAGAGGGGC CCGAAGTCAC AGATCCTCT TCTGGAGAAA AGAGTCTAGC CCGAAGTCAC AGATCCTCT AAAGGAGACA TTCCCAGGAC TCCCAGGAC TCCCAGGAC TTCCCACGAC TTACTTATT 1320 778 AAGAGGGGG CCGAAGTCAC AGATCCCTC AAAGGAACAA TTCCCACGAG TCCCACGAGC TCCCAGGAC TCCCAGGAC TCCCAGGAC TCCCAGGAC TCCCACGAC TTCCCTCTGC TCCCTTAGAC AGACCCACC TACCACCAC TCCCAGGAC TTCCCACGAC TTCCCTCTGC TCCCTTAGAC AGACCCACCC TACCACCAC TCCCAGGAC TCCCAGGAC TCCCACCACACAC TCCCACCACACAC TCCCACCACACAC TCCCACCACACAC TCCCACCACACACA	763 CARAGIARAG CITTATATA GAATGCAGCC ACTTTTGGAG GTGCTATCCA TTC11CAGT	
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770 AGCATCTCTT CAGGAGGTCC TATTGC CATTGATACT GGAGGGGAGA TCAGTTATC AGCAGAGAAA TO ATTTTAGGTG GAGCTATTGC CATTGATACT GGAGGAGAAT TTTTAGATGG CATCCATCTT TTTTAGATGG CATCCATCTT TTTTAGATGG CATCCATCTT AGAATTTATA TTACAAAATG CTAAAATTCCT GAAATTACAG GCGAGAAATG GATGCTCTATA AGAATTTATA CACTCAGAGC CATTACTCTTT TCTGGAGAAA AGAGTCTAGC AAACGATCCT TCTGGAGAAA AGAGTCTAGC AAACGACCCT CTGCAGGATA ATTTAGATTTA AATCTACAAT CCCCACTGT CTGCAGGATA CTTAGTTTATTA AATCTACAAT CCCCACTGAAAA TTCACAGAC GATACCCTCT AAGGAAGAAA TTCACAGAC GAACCAAACT GATACCCTCT AAGGAAGAAA TTCACAGAC GAACCACACC AAAGAACACGCA AAAGAACACGCA AAAGAACACGCA AAAGAACACGCA AAAGAACACGCA TTCACAACAC TTATTAAAGC AAACACCGCA TTCCCTCTGC TCCTCTGC CAATGCCTAT TCCCTCTGC TCCTCTTTAGA ATCCCTCAC AAAGAACACGCC TCCCTCTGC CAATGCCTAT TCCCTCTGC TCCTCTTTAGAAC AAACACCGCA TTCCCTCTGC TAAATCCCTCTATA TCCCTCTCGC TCCTCTCTGC CAATGCCTAT TCCCTCTGC TCCTCTTTAGAAC AAACACCGCA TTCCCTCTGC TCCTCTTTAGAAC AAACACCGCA TTCCCTCTGC TCCTCTTTAGAAC AAACACCGCA TTCCCTCTGC TCCTCTTTAGAACACACGCC TCCCTGGAGCC TCCCTCTGC TCCTCTTTAGAACACACGCC TCCCTCTGCT TAAACTCCTCTCTAAAACACACGCAC TCCCTCTCTGC TCCTCTCTGC TCCTCTTTAGAACACACACACACACACACACACACACACA	768 CTTCCCACT CAGGARACTA TTCCATAATG GGTGGCGGAG CCATTTATGC TAGGARACTA	
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772 GGAACAATTA CATTCCAAGG AAACGGACATTA GAAATTACAT TATATATATATATATATA CATTCCAAGG AGATGGAAAATG GAACACAGGAAATG AAACGACCCTAAAA AGAGTCTAAA ATATCAACAG AGATGGAACA ACCCAATTGA ATATCAACAG AAACGACCCTA AAACGACCCTA AAACGACCCTAAAAAAAAAA	770 AGCATCHTT CAGCATATTGC CATTGATACT GGAGGGGAGA TCAGTTTATC AGCAGAGAAA	
773 TTACAAAATG CTATATCCT GAAGC AGATGGTCT ACCCAATTGA ATATCAACGG AGATCCTAAA 774 GATCCTATTA CTTCTGAAGC AGATGGGTCT ACCCAATTGA ATATCAACGG AGATCCTT 775 AATAAAGAGT ACACAGGGAC CATACTCTTT TCTGGAGAAA AGAGTCTAGC AAACGATCCT 776 AGGGATTTA AATCTACAAT CCCCTCAGAAC 777 AAAGAGGGG CCGAAGTCAC AGTTCCAAAA TTCACGCAGT CTCCAGGATC CTTATGTTT 777 AAAGAGGGGG CCGAAGTCAC AGTTCCAAAA TTCACGCAGT CTCCAGGATC AGGCCTGCG 778 TTAGATATAG ATACCTAAC GATAGCCTCT AGGCAAGACA TTCCCTACAC AGGCCTCGCG 779 ATAGATATAG ATACCGTGAC GGACTCTATA ACACCACGCA TCCCTTATAAACCAGA TTCCCTACACAC GAATGACACCGCA 781 GAAGATCTCA GAATGAGAAA TTCACAGACG TCCCTATGCCTATT 782 GGGGGTAGT TGACTGTAAC TCCTGAGACA TTCCCTCTGC TAAGTCCCCA TTATGGTTTT 783 CAAGGCAATT GGAAATTAGC TTGGAGAAC ACAGCACGC TCCTTTAGAACACACCACAC	771 AATTTAGGTG GAGCTATCAAGG AAACCGGACG AGCTTACCGT TTTTGAATGG CATCCATCT	
774 GATCCTATTA CTTCTGAAGC AGATGGOT TCTGGAGAAA AGAGTCTAGC AAACAGTCCT 775 AATAAAGAGT ACACAGGGAC CATACTCTTT TCTGGAGAAA AGAGTCTAGC AAACAGCACTCT 776 AGGGATTTTA AATCTACAAT CCCTCAGAAC GTCAACCTGT CTGCAGGATC CTATAGTTATT 777 AAAGAGGGGG CCGAAGTCAC AGTTTCAAAA TTTCACGCAGT CTCCAGGATC GCATTAGTT 778 TTAGATTTAG GAACCAAACT GATAGCCTCT AAGGAAGACA TTGCCATCAC AGGCCTCGCG 779 ATAGATATAG ATAGCTTAAG CTCATCCTCA ACAGCAGCTG TTATTAAAGC AAACACCGCA 780 AATAAACAGA TATCCGTGAC GGACTCTATA GAACTTATCT CGCCTACTGG CAATGCCTAT 781 GAAGATCTCA GAATGAGAAA TTCCACAGACG TTCCCTCTGC TCTCTTTAGA GCCTGGAGCC 782 GGGGTAGTG TGACTGTAAC TGCTGGAGACA ACTGCAGACA ATTGTTCTGGAAGACA AAAGAAGACA ATTTTCGATGAACAA AAAGAACACACCA TGCATCGGC 783 CAAGGCAATT GGAAATTAGC CAGATCCTTA ATGCAGAGCA ATTTTCTCGAAGACA ATTTCCACAGACA ATTTCCATCA AAAGAAGACA ATTTCCAAGACA ATTTCCGATGA AAAGAAGACA ATTTCCAACAA CGAATCACAC CAATGAATAT TTCCGTTATA GGAACTATTTTCCAACAA ATTTCCGTTAT TCCAACAA ATTTCCGTTAT TCCAACAACA CTAAACACAC CAATGAATAT TTCCGTTAT TCCAACAA ACCCTCAATGT TAACACTTTTA GAACACACC CTAAACACAC CAATGAATAT TTCCGTTAT TCCATCAGAT TTCCCTATGGT TAACACTTTTT TCCATTATT TCCATTATTTT TCCATTATTTT TCCATTATT TTCCATTATT TCCATTATTTT TCCATTATTT TCCATTATTTT TCCATTATTTTT TCCATTATTTT TCCATTATTTT TCCATTATTTT TCCATTATTTT TCCATTATTTT TCCATTATTTT TCCATTATTTT TCCATTATTTT TCCATTATTTTT TCCATTATTTTTT TCCATTATTTTTT TCCATTATTTTTT TCCATTATTTTTTTT	772 GGAACAATTA CATACCT GAAATTACAG GCGAGAAATG GATGCTCTAT AGAATTIAL	
775 AATAAAGAGT ACACAGGAC CITACTOT CTGCAGGATA CTTAGTTATT 776 AGGGATTTTA AATCTACAAT CCCTCAGAAC GTCAACCTGT CTGCAGGAT CTTAGTTAGTT 777 AAAGAGGGG CCGAAGTCAC AGTTTCAAAA TTCACGCAGT CTCCAGGAT AGGCCTCGCG 778 TTAGATTTAG GAACCAAACT GATAGCCTCT AAGGAAGACA TTGCCATCAC AGGCCTCGCC 1440 779 ATAGATATAG ATACCGTGAC GGACTCTATA GAACTTAATCT CGCCTACTG CAATGCCTAT 1560 780 AATAAACAGA TATCCGTGAC GGACTCTATA TTCCCTCTGC TCTCTTTAGA GCCTGGAGC 1620 781 GAAGATCTCA GAATCAGACA TTCCACAGACG TTCCCTCTGC TCTCTTTAGA GCCTGGAGC 1620 782 GGGGGTAGTG TGACTGTAAC TGCTGGAAACA AAGTTGGAA ATTCTTCTGG AAAGAACAA AAGTTGGAGA ATTCTTCTGG AAAGAACAA AAGTTGGAAACA ATTCTTCGATG GCATTTTCC TAAATATCTT GAAAATCAC TTACTTTCA TGCATCAC TTATTATATCT TGTAAATATA ATTTCCATACA CCTAAGCACTA ATCTTCACAGAC ACCCTTATA TTCCAGAGACA ACCCTTATA TTCCAAGACA ACCCTTATA TTCCATCAGA AACTTTTAG TAGAGACAAA 1980 785 TGGGGGAACA ATTAAAGGTA CGGAATACAAA AGGGGTGGAT ATCTTCTCA TGTAAATAT 1980 786 TACAGACACA CTAAAGCAC TACTTCGATG GCATTTTCC AACTCTTATA TTCCATTAGTTT TTCATATTTT TTCATAATAT 1980 787 TCCGAAGACA ATTAAGGTA CGGAATACAGA ATTTTTCCGTTAT TTCCATTAT TTCATATTTT TTCATATATCT CTACAATAT 1980 788 GAGATCACC CTAAGCACTA ATCTTCGATG GCATTTTTCC AACTCTTAT TTCCATTAT TTCCATTATT TTCATTTTTT TTCATATATTT TTCATTTTTT TTCATATATTTT TTCATATTTTT TTCATATTTTT TTCATATTTTT TTCATATTTTTT TTCATATTTTTTTT	773 TTACARART CITACTGAAGC AGATGGGTCT ACCCAATTGA ATATCAACGG AGATCCIARA	
776 AGGGATTTTA AATCIACAT 777 AAAGAGGGGG CCGAAGTCAC AGTTTCAAAA TTCACGCAGT CTCCAGGATC GCATTAGTT 778 TTAGATTTAG GAACCAAACT GATAGCCTCT AAGGAAGACA TTGCCATCAC AGCCCTCGCG 779 ATAGATTAG ATACCGTGAC GATAGCCTCTA ACACCAGCTG TTATTAAAGC CAATGCCTAT 780 AATAAACAGA TATCCGTGAC GGACTCTATA GAACTTATCT CGCCTACTG CAATGCCTAT 781 GAAGATCTCA GAATGAGAAA TTCCACAGACG TTCCCTCGC TCTCTTTAGA GCCTGGAGCC 782 GGGGGTAGTG TGACTGTAAC TTGCACAGACG TTCCCTCTGC TAAGTCCCCA TTATGGTTTT 783 CAAGGCAATT GGAAATTAGC TTGGACAGGA ACTGGAAACA AAGTTGGAGA ATTCTTCTGG 784 GATAAAATAA ATTATAAGCC TAGACCCTGA AAAGAACAA AAGTTGGAGA ATTCTTCTGG 785 TGGGGGAATG CTGTAAATGT CAGACCCTAA AAAGAACGAA AAGTTGAGACA ATTATCTTCCG 786 TTACAGACAG ATTGAGGACA ATTATAGGCC GAGATCCTTA ATGCAGGACA ATTCTTCCA TGTATCTCCC 787 TCCGAAGACA ATTAAGGTA CGTATACACAGA ATGTTTTCCA ACACTCTTAG TAGAGACAAG ACTCTTTAG TAGAGACAAG CCTAAGCACTA TACTTCGATG GCATTTTCCA ACACTCTTAT TTCCAATAT TTCCATTATC TTATAAATAT 1980 787 ACACCCTCC TAGGGAATAT TTTCCAACAA ATTTTTTCGTTAT TTCCATTTTT TTCAAAATAT 1990 788 GAGATCACAC CTAAGCACTA TACTTCGATG GCATTTTCCA ACACTCTTAG TAGAGACAAG ACCTTTTAG TAGAGACAAG ACCTCTTAT TTCCAACAA ACCTCTTAT TTCAAAATAT 1990 789 ACAACCTCCC TAGAGCACTA TACTTCGATG GCATTTTTCC ACCTAATGT AAACGTCGGG 1200 790 ACAACCTCCC TAGGGAATAT TTTCCGTTAT TTCCATTTTT TTCAAAATACC CTTATGATTT TTCCATTATTT TTCCAAAATAC 2220 791 ATTCTCCAACA ATTGTTGGC TAAAACAGAC TACACTATAT TTCCCTTATT TTCCATTTTT TTCCAAAAACAC CAACCACTATTTAGAAC AACCTCTAAT GGAAAACAGC 1200 792 GGTCATGCCA CCAATGATAT TTCCACAGA ATTCTTTTTT TTCCAAAAACAC CAACCACTATTTTTTTT	774 GATCCTATTA CITCLEGGAC CATACTCTTT TCTGGAGAAA AGAGTCTAGC AAACGATCT	
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792 GGTCATGCCA CCAATGATAT GAAAACAGTGC GGAGGGAGCA TGCCTCTATT GGTATTTGAG 793 TGGAGAAACA ATTGTTGGGC TATAGAGTGC GGAGGGAGCA TGCCTCTATT GTATGCTTAT 2400 794 AACGGAAGAC TTTTCCAAGG TGCCATCCCA TTTATGAAAC TACAATTAGT TTATGCTTATACA	790 ACAACCTCCC TAGGGATTCT TCAAAATCCT CTTATGATTT TTCATTTTTT GTGTGTTAT	_
793 TGGAGAAACA ATTGTTGGGC TATAGACTCA TTTATGAAAC TACAATTAGT TTATGCTTAT 2400	791 ATTOTICICA CAAGGITAT GAAAACAGAC TACGCAAATT TCCCTATGGT GAMAACAGC	
794 AACGGAAGAC TTTTCCAAGG IGCCATCOOL TOTAL	792 GGTCATGCCA CCARGETTGGGC TATAGAGTGC GGAGGGAGCA TGCCTCTATT GGTATTTGAG	
794 AACGGAAGAC TITTCAGAGAGAC GACTGCAGAT GGCCGTAGAT TTAGTAATGG GAGTTTAACA 2400 795 CAGGGAGATT TCAAAGAGAC GACTGCAGAT GAGAAGCTGG CACTTTCTCA GGATGTACTC 2520 796 TCGATTTCTG TACCTCTAGG CATACGCTTT GAGAAGCTGG CACTTTCTCA GGATGTACTC	793 TGGAGAAAA ATIGITAGG TGCCATCCCA TTTATGAAAC TACAATTAGT TTATGCTTAT	
795 CAGGGAGATT TOTAL TACCTCTAGG CATACGCTTT GAGAAGCTGG CACTTTCTCA GGATGTACTC 2220	794 AACIGGAGAC TITTECCATACA GACTGCAGAT GGCCGTAGAT TTAGTAATGG GAGTTTAACA	
796 TCGATTTCIG IACCIOINGS STATE	795 CAGGGGGATT TACCTCTAGG CATACGCTTT GAGAAGCTGG CACTTTCTCA GGATGTACTC	2220
	796 TUGATITUTE INCOLUMN	

number of bases

conflict, 3052 listed, 3051 four

RAW SEQUENCE LISTING DATE: 09/06/2000 TIME: 11:01:37

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Output Set: N:\CRF3\09062000\1446677.raw

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                                                                                     2640
     799 TTTGTAGGGA GTGGAACGGG TCGGTATCAC TTTAACGACT ATACTGAGCT CTTATGTCGA
                                                                                      2700
     800 GGAAGTATAG AATGCCGCCC CCATGCTAGG AATTATAATA TAAACTGTGG AAGCAAATTT
801 CGTTTTTAGA AGGTTTCCAT TGCCTGTGT GTTCCGGATC TTAACTATAA ATCCTGGACT
                                                                                      2760
                                                                                      2820
     802 ATGGATCATA GGCATTGGGT TTCTCGAACT TGTGTGGAGA ATAACGACAT TTTATATGCA
                                                                                      2880
     803 TAACGGAATA CTCGTATCAC CTCAGCCCCT AGAGACATTC TTTAGGGGTT CTTTATTTGT
                                                                                      2940
     804 CTAAACTTCG TATTTTATCG AGAATCCTTT ACGTTCTTGG TTTGCTTGTC TCCGAGGAGT
                                                                                      3000
E--> 805 TCTCTAACGA ATCATAGGGA TTCCAGGGTT CTGTTCCTTG AGTCCTTTGG A
                                                                                      (3052)
     2597 (2) INFORMATION FOR SEQ ID NO: 24:
                 (i) SEQUENCE CHARACTERISTICS:
     2599
                       (A) LENGTH: 946 amino acids
(B) TYPE: amino acid
                                                       ->> See p.6
      2600
      2601
                       (C) STRANDEDNESS: single (D) TOPOLOGY: linear
      2602
      2603
                (ii) MOLECULE TYPE: peptide
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
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      2609 Met Lys Thr Ser Val Ser Met Leu Leu Ala Leu Leu Cys Ser Gly Ala
2610 1 5 10
      2612 Ser Ser Ile Val Leu His Ala Ala Thr Thr Pro Leu Asn Pro Glu Asp 2613
            Gly Phe Ile Gly Glu Gly Asn Thr Asn Thr Phe Ser Pro Lys Ser Thr 40 45
      2615
      2618 Thr Asp Ala Ala Gly Thr Thr Tyr Ser Leu Thr Gly Glu Val Leu Phe 2619 50 60
      2017 30 30 2621 Ile Asp Pro Gly Lys Gly Gly Ser Ile Thr Gly Thr Cys Phe Val Glu 2622 65 70 75 80
       2624 Thr Ala Gly Asp Leu Thr Phe Leu Gly Asn Gly Asn Thr Leu Lys Phe 2625 85 90 95
       2627 Leu Ser Val Asp Ala Gly Ala Asn Ile Ala Val Ala His Val Gln Gly
2628 100 105
       2630 Ser Lys Asn Leu Ser Phe Thr Asp Phe Leu Ser Leu Val Ile Thr Glu
2631 115
       2633 Ser Pro Lys Ser Ala Val Ser Thr Gly Lys Gly Ser Leu Val Ser Ser 2634 130 135 140
       2636 Gly Ala Val Gln Leu Gln Asp Ile Asn Thr Leu Val Leu Thr Ser Asn 160 2637 145
       2639 Ala Ser Val Glu Asp Gly Gly Val Ile Lys Gly Asn Ser Cys Leu Ile
2640 165 170
        2642 Gln Gly Ile Lys Asn Ser Ala Ile Phe Gly Gln Asn Thr Ser Ser Lys
2643 180 185 190
        2645 Lys Gly Gly Ala Ile Ser Thr Thr Gln Gly Leu Thr Ile Glu Asn Asn
2646 195 200 205
        2651 Ala Leu Asp Leu Gly Ala Ala Ser Thr Phe Thr Ala Asn His Glu Leu 2652 225 230 240
        2654 Ile Phe Ser Gln Asn Lys Thr Ser Gly Asn Ala Ala Asn Gly Gly Ala
                                245
```

DATE: 09/06/2000 TIME: 11:01:38

Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I446677.raw

2657 Ile Asn Cys Ser Gly Asp Leu Thr Phe Thr Asp Asn Thr Ser Leu Leu 2660 Leu Gln Glu Asn Ser Thr Met Gln Asp Gly Gly Ala Leu Cys Ser Thr 2661 275 280 285 2666 Thr Ser Gly Gln Lys Gly Gly Ala Ile Ser Ala Ala Ser Leu Lys Ile 2667 305 310 315 320 2669 Leu Gly Gly Gln Gly Gly Ala Leu Phe Ser Asn Asn Val Val Thr His 32670 325 330 335 2672 Ala Thr Pro Leu Gly Gly Ala Ile Phe Ile Asn Thr Gly Gly Ser Leu 340 340 2675 Gln Leu Phe Thr Gln Gly Gly Asp Ile Val Phe Glu Gly Asn Gln Val 2676 355 360 2678 Thr Thr Thr Ala Pro Asn Ala Thr Thr Lys Arg Asn Val Ile His Leu 375 380 2681 Glu Ser Thr Ala Lys Trp Thr Gly Leu Ala Ala Ser Gln Gly Asn Ala 2682 385 390 395 2684 Ile Tyr Phe Tyr Asp Pro Ile Thr Thr Asn Asp Thr Gly Ala Ser Asp 2685 405 410 2687 Asn Leu Arg Ile Asn Glu Val Ser Ala Asn Gln Lys Leu Ser Gly Ser
420
425
420
427 2693 Asn Leu Thr Ser Arg Ile Asn Gln Pro Val Thr Leu Val Glu Gly Ser 2694 450 455 2694 430 2696 Leu Glu Leu Lys Gln Gly Val Thr Leu Ile Thr Gln Gly Phe Ser Gln 480 2697 465 470 2699 Glu Pro Glu Ser Thr Leu Leu Leu Asp Leu Gly Thr Ser Leu Gln Ala 2700 485 490 495 2702 Ser Thr Glu Asp Ile Val Ile Thr Asn Ser Ser Ile Asn Ala Asp Thr 505 510 2705 Ile Tyr Gly Lys Asn Pro Ile Asn Ile Val Ala Ser Ala Ala Asn Lys 520 525 2708 Asn Ile Thr Leu Thr Gly Thr Leu Ala Leu Val Asn Ala Asp Gly Ala 2709 530 540 2711 Leu Tyr Glu Asn His Thr Leu Gln Asp Ser Gln Asp Tyr Ser Phe Val 2712 545 2714 Lys Leu Ser Pro Gly Ala Gly Gly Thr Ile Ile Thr Gln Asp Ala Ser 2715 565 570 2717 Gln Lys Leu Leu Glu Val Ala Pro Ser Arg Pro His Tyr Gly Tyr Gln
2718 580 580 2720 Gly His Trp Asn Val Gln Val Ile Pro Gly Thr Gly Thr Gln Pro Ser 605 2723 Gln Ala Asn Leu Glu Trp Val Arg Thr Gly Tyr Leu Pro Asn Pro Glu 2724 610 615 2726 Arg Gln Gly Phe Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Val Asp 640 2727 625 630 630 2729 Gln Arg Ala Ile Gln Glu Ile Met Val Asn Ser Ser Gln Ile Leu Cys FIT (11/1/E)

DATE: 09/06/2000 TIME: 11:01:38

Input Set : A:\Birkell.txt
Output Set: N:\CRF3\09062000\I446677.raw

```
2732 Gln Glu Arg Gly Val Trp Gly Ala Gly Ile Ala Asn Phe Leu His Arg 670
2735 Asp Lys Ile Asn Glu His Gly Tyr Arg His Ser Gly Val Gly Tyr Leu
2736 675 680
2738 Val Gly Val Gly Thr His Ala Phe Ser Asp Ala Thr Ile Asn Ala Ala 2739 690 695
2741 Phe Cys Gln Leu Phe Ser Arg Asp Lys Asp Tyr Val Val Ser Lys Asn 720 2742 705 - 710 - 720
2744 His Gly Thr Ser Tyr Ser Gly Val Val Phe Leu Glu Asp Thr Leu Glu 735 730 735
2747 Phe Arg Ser Pro Gln Gly Phe Tyr Thr Asp Ser Ser Glu Ala Cys
750
748
2750 Cys Asn Gln Val Val Thr Ile Asp Met Gln Leu Ser-Tyr Ser His Arg
2751 755 760 765
2753 Asn Asn Asp Met Lys Thr Lys Tyr Thr Thr Tyr Pro Glu Ala Gln Gly
2754 770 780
 2756 Ser Trp Ala Asn Asp Val Phe Gly Leu Glu Phe Gly Ala Thr Thr Tyr 795 785 785
 2759 Tyr Tyr Pro Asn Ser Thr Phe Leu Phe Asp Tyr Tyr Ser Pro Phe Leu 815 805
 2762 Arg Leu Gln Cys Thr Tyr Ala His Gln Glu Asp Phe Lys Glu Thr Gly 825
  2765 Gly Glu Val Arg His Phe Thr Ser Gly Asp Leu Phe Asn Leu Ala Val
2766 835
  2768 Pro Ile Gly Val Lys Phe Glu Arg Phe Ser Asp Cys Lys Arg Gly Ser 2769 850 860
  2771 Tyr Glu Leu Thr Leu Ala Tyr Val Pro Asp Val Ile Arg Lys Asp Pro 2772 865
  2774 Lys Ser Thr Ala Thr Leu Ala Ser Gly Ala Thr Trp Ser Thr His Gly 895 2775
  2777 Asn Asn Leu Ser Arg Gln Gly Leu Gln Leu Arg Leu Gly Asn His Cys 910 900 910
  2780 Leu Ile Asn Pro Gly Ile Glu Val Phe Ser His Gly Ala Ile Glu Leu
2780 - 915 920 925
   2783 Arg Gly Ser Ser Arg Asn Tyr Asn Ile Asn Leu Gly Gly Lys Tyr Arg
2784 930 935
   2786 Phe
```

945 amino acids found, 946 listed as length.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/446,677

DATE: 09/06/2000

TIME: 11:01:39

Input Set : A:\Birkel1.txt
Output Set: N:\CRF3\09062000\I446677.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:38 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:510 M:320 E: (1) Wrong Nucleic Acid Designator, 2
L:805 M:254 E: No. of Bases conflict, Input:3052 Counted:3051 SEQ:5
L:805 M:204 E: No. of Bases differ, LENGTH:Input:3052 Counted:3051 SEQ:5
L:2454 M:220 C: Keyword misspelled or invalid format, [(ii) MOLECULE TYPE:]
L:2787 M:203 E: No. of Seq. differs, LENGTH:Input:946 Found:945 SEQ:24